

Fig. 1

HP02573 61' YGRQDLHLRIFDPSPIEDARADNI FTATERNRIDYVSSAVRIDHAPDLPRPEVCFIGRSN
 Cgpa 1"* * * * *
 MFFAQPVSFIMGAVRMDAMPSPDLPEVAFAGRSN

HP02573 121' VGKSSLIKALFSLAPEVEVRVSKKPGHTKKMNFVKVGHFTVVDMPGYCF----RAPED
 Cgpa ***** * * * * *
 ***** * * * * *
 ***** * * * * *

HP02573 176' FVDMVETYLKERRNLKRFTLLVDSVVVGIQKTDNIAIEMCEEFALPYVIVLTKIDKSSKGH
 Cgpa * * * * *
 * * * * *
 * * * * *

HP02573 236' LLKQVLQIQKFVNMKTQGCFFPQLFPVSAVTFSGIHLRCFIASVTGSLD
 Cgpa * * * * *
 * * * * *

HP02573 153" VDKVVAETQKAIKRAAA-FPRVLATSSSEKGLGMPRELRAEIVRLCIDE

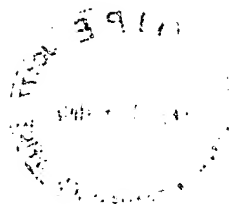


Fig. 2

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HP02612 61' KVPLAGGGRKPRHLHRRHRVYKLVEDTKHRPKENLELILTQSVENVGVRGDLVSVKKSGLGR
          ***** ** * ** * **
          MKLILTADVVDHGLGSVGDITVEVKDGYGR

RL9_MYCLE 1"

HP02612 121' NRLLPQGLAVYASPENKKLFEEEKLLRQEGKLEKIQTKAAGEALGVVVAPHTYKLPAPETIT
          * * * * * . . . . . * * * * . . . . . * * * * . . . . .

RL9_MYCLE 28" NFLLPHGLAIVASRGAQQADEIRRAR-ETKAMRDREHANEIKVAIEALGSVSLPMKTVA

HP02612 181' RWGEYWCETVNGLDTVRVPMVSVNFEKPKTKRYKWLAQQAAKAMAPTSPQI
          * . . * * . . . . . * * * * . .

RL9_MYCLE 87" DSGKLFGSVTAGDVVAI KKAAGPNLDKRIVRLPKTHIKAVGTHPVSVHLHPEVDVVVLL

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Fig. 3

HP10117	61'	KAKGQSQTRVNINAALVEDIINLEEVNEEMKSVIEALKDNFNKTNLNIRTPSGSLDKIA ..* *.....***..... .*.***.*.*.
RRF_BRUME	1"	MSDAFDINDLKRMEGAVNALKHDLGLRTGRASASLLPEPIT
HP10117	121'	VVTADGKLAINQISQISMSPQLILVNMASFPECTAAAI-KAIRESGMNLNPEVEGTLLR**....** * ***...*** . . *
RRF_BRUME	43"	IEAYGSTMPINQVANISV--PESRMLSVSVWDKSMVGAVERAIRDSGLGNLPITDGMTLR
HP10117	180'	VPIPQVTRHREMLVKLAQNNTNKAKDSLKVRTNSMNKKK-SKDT-VSEDTIRLIEKQ* ..***.* ..* ..* ..* ..* ..* ..* ..* ..* ..*
RRF_BRUME	101"	IRLPELNEQRRELKLVKIAHQYAEQGRIARHVRRDGMQDLKLEKDSVISQDESRLVSEK
HP10117	238'	ISQMADDTVAEIDRHHLAVTKELLG***...***.*..
RRF_BRUME	161"	VQKLTDTTIAEMDKIVAVKEGEIMQV

Fig. 4

HP10120 1' MQRVSGLLSWTLRVLWLSGLSEPGAARQPRIMEE-KALEVYDLIRTIRDPEKPNLLEEL
CEF45G2 1" MGQERLDNANPTLFDSKPRHRPVTGTERDESVEPDFDSWEIFDLIRDINDPEHPYTLLEQL
HP10120 60' EVVSESCVEVQEINEEYLVIIIRFTPTVPHCSLATLIVGNLHF
CEF45G2 61" NVVQEELIKV-FIDEETFVKVNFPTTIPHCSMATLIGLAIRVKLLRSLRHPKVKVSVSIT

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Fig. 5

[illegible]

Fig. 6

HP10582	1'	MDSNHQSNYKLSKTEKKFLRKQIKAKHTLLRHE-GIETVSYATQSLVVANGGLGN
YKY5_CAEEL	361"	RELSYFNEEKAKRIGERFEGGKLAKKVHKSIEQLKRHPDVQISTEPTKYLLVSNSSILC
HP10582	55'	GVS RNQLLPV-LEKCGLV DALLMPPNKPYSFARYRTTEESKRAYVTTLNGKEVVDLGGQKI
YKY5_CAEEL	421"	GVSLEELEEIFLPLDELAEFIVYPNKRYSFVQCSSIEKSIQVRTELHGLIPPSLKNSHQ
HP10582	114'	TLYLNFVEKVQWKELRPQALPGLMVVEEIIISSEEEKMLLESVDWTDTDNQNSQKSLKH
YKY5_CAEEL	481"	PFAISYVENLPEATKCEDFRPANLKIIEEYVSSDLEKELVDLV-----TNHPSVQSLKH
HP10582	174'	RRVKHFGYEFHYENNVDDKDKPLSGGLPDICESFLEKWLKGYIKHKPDQMTINQYEPGQ
YKY5_CAEEL	535"	RAVHFGHVFDYSTNSASEWKE-ADPIPPVINSLIDRLISDKYITERPDQVTANVYESGH
HP10582	234'	GIPAHIDTHSAFEDEIVSLSLGSEIVMDFKH--PDGIAVPVMLPRRSLLVMTGESRYLWT
YKY5_CAEEL	594"	GIPSHYDTHSAFDDPIVSI SLLSDVVMFEFKDGANSARIAPVLLKARSLCLIQGESRYRWK
HP10582	292'	HGITCRKFDTVQASESLKSGIITSDVGDDLTLSKRGLRTSFTFRKVRQTPCNCYSPLVCDS
YKY5_CAEEL	654"	HGIVNRKYD-----V-----DPTNRVVPRQTRVSLTLRKIRKPCCEWKEFCDW

...and the

Fig. 6-1

[illegible]

Fig. 7

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HP10149	1'	MAMSFEPWQYRFPFFFTLQPNVDTRQQLAAWCSLVLSEFCRLHKQSSMTVMEA
W02A11	1"	MAAATTTASAFKWPWQYDFPFFFTIQKSINTKDKQLEAWARLVIDYAQHKNKIYSLDIAEA
HP10149	55'	QESPLFNNVKLQKLPVESIQIVLEELRKKGNLEWLDKSKSSFLLIMWRRRPEEWGKLIYQW
W02A11	61"	TTSELFNNQKLNRRRLSTDGVNTVLQYLEQKKLIEFTDNGRTRFRHFWRRRPDVWANMIYQW
HP10149	115'	VSRSGQNNSVFTLYELTNGEDTEDEEFHGLDEATLLRALQALQOEHKAEIITV-SDGRGV
W02A11	121"	AVENAFINTPLTYEITHGDDTTNESFHNLEREILMKALTCLEEQRRRAQLMNIIGDNEGV
HP10149	174'	KFF
W02A11	181"	KFI

Fig. 8

HP10160 1' MASRGKTETSKLKQNLQEQDLRLMQQLQDLQECREELDTDEYETKKTETLEQLSEFNDSL
 ZK1248 1" MGVDLLIKNAQKTIDRLIRQLAEIEQEEENNLEDEYRELREDTVNLQEQYQKIV
 HP10160 61' KKIMSGNMTLVDELSGMQLAIQAAISQAFKTPVIRLFAKKQPGQLRTRLAEMDRDLMVG
 (ZK1248 56" ERLQGGDVSLIDDLTATKIAIRMAISKAFTKTPHMAITAGZHTGLLREKLMNTETNYRSQ
 HP10160 121' KLERDLYTQQKVEILTALRKIGEKLTADEAFLSANAGAILSQFEKRVSTDLGSGDKIILAL
 ZK1248 116" KMPKQGYLERKFEILMALRRLEETLTEDERKFLSDRLET--PEFQLIEANANRLFSGNVT
 HP10160 181' ASFEVEKTKK
 ZK1248 174" SPVFRVQIMASPKPKKVRLLDDKTENVSPPKAWHTTEKKRKFYTNDKTKESLWDHPNTR

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Fig. 9

HP10173 1' MKLLTHNLLSSHVRGVSGRGFFPLRLQATEVRICPVFNPNFVARMIPKVEWSAFLEAADN
C04H5 1" MKLFFVHNFMSSRFLKNVTGVYPLNLVVKQFVEKDIEFDRDNTIVMLDRIQYEALIVAAAA

HP10173 61' LRLIQ-VPKGPVEGYEE-NEEFLRTMHLLLEVEVIEGTLCPESGRMFFPISRGI PNMLL
C04H5 61" VNQSDRIPREKPEKWDELTDQLRVFHHLLMNIDVIDGELICPETKTTFPIRDGIPNMLK

HP10173 119' SEETES

..*

C04H5 121" VDAEK

(continued)

[illegible]

Fig. 10-1

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HP02644 300' DDVIESEALPSDIAEFARAKTGGTVSDQALLFGDDDAGEGPSSLIREKPVPKQNEEEEE
CELLF55F8 263" -----

HP02644 360' NLDKEQTGNLKQELDDKSATCKAYPKRPILGLVLTPFRELA VQVKQHIDAVARFTGIRTA
          *...*****...***. * . . .
CELLF55F8 323" -----ALIVAPTRRELVIQIMKHINALISTTQLIAT

HP02644 420' ILVGGMSTQKQOFML-NRRPEIVVATPGRLWELIKEKHY--HLRNLRLQLRCLVVDADRML
          ***. **... ..**.*...*****...* . . .*.*****.***
CELLF55F8 383" STVGGLAQVKQERIISQORPDI VVATPGRLWAMMOJEAETGEFLAEMKDLKCLVVDETDRM

HP02644 477' VEKGHPAELSQILLEMLNDSQYNPKRQTLVFSATLTLVHQAPARILHCKHTKQMDKTKAKLD
          **.*...*****...* *...*****...* . . .*.*****.***
CELLF55F8 443" VEEGYFAELTHILINKIHEESEKEKELQTLVFSATLTFKAQDVAEFEKKKAKELSSQOKIQ

HP02644 537' LLMQKIGMR-GKPKVIDLTRNEATVETLTETKIH CET-DEKDFLYYFLMQYPGRSLVFA
          **.*...*.*****...*...*...*...*...*...*...*...*...*...*...
CELLF55F8 503" RLILKLTGLRENKHVIDLTRQMGTAGCLVEARINCGNLLERKDTSLVYLLTRYPGRTIVFV
  
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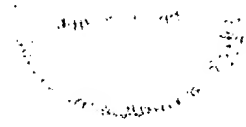




Fig. 10-2

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HP02644 595' NSISCIKRLSGLLKVLVDIMPLTLHAOMHQKORLRNLQFARLEDCVLLATDVAARGLDIP
***. ** ..** ..* *..*** * *****.***. * .. *****
CELF55F8 563" NSIDAARRLYSVLKSVNIDPMILHAKMIQKORLKNLEKFSSEKNAVLLATDVAARGLDIQ
.. *****. ***. *****.***. *****.***. * .. *****.***.
HP02644 655' KVQHVTHYQVPRTSEITYVHRSGR TARATNEGLSLMLIGPEDVINFKKIYKTKKDEDIPL
.. *****. ***. *****.***. *****.***. * .. *****.***.
CELF55F8 623" GIDBVIHYQVPKKVEITYIHRSGRTARASHERGLTVVLVDPPSRQFYMKLCKGLNPMQDLNV
.. *****. ***. *****.***. *****.***. * .. *****.***.
HP02644 715' FFPVQ-TKXMDVVKERIRLARQIEKSEYRNFOACLENWIEQAAALEIELEEDMKKGKA
***. * ..**..**..***.***.***. * ..**..***. * ..**..***. * ..**..***.
CELF55F8 683" FPIDFEPLMNAIKKRVRLASEIDSLGFRCKKIKMSESWFEKARAADILDYDETRHREMDG
.. *****. ***. *****.***. *****.***. * ..**..***. * ..**..***.
HP02644 774' DQQEERRRQKQMKVLKCELRLHLLSQPLFTESQKTKYPTQSGKPPLLVSAPSKSEALSCL
. * ..**..**..**..**..**..**..**..**..**..**..**..**..**..**..**..
CELF55F8 743" LNLEVDIMVQKSRQLQAQLRTLSLPLPRVDGSDSMKTKYITPEIVARLSVGDNAIDVL
.. *****. ***. *****.***. *****.***. * ..**..***. * ..**..***.
HP02644 834' S-KQKKKKTKKPKPEQPEQPQSTSAN
. * ..**..**..**..**..**..**..**..**..**..**..**..**..**..**..**..
CELF55F8 803" NQKIDETKEWKPKSRKATREDEENSMCKSLKSSQKKEKRLAEKKKQKQKAAKVTKLSETD
.. *****. ***. *****.***. *****.***. * .. *****.***.

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Fig. 11

[illegible]

HP10437 1' MQKSCSENEGKPNMPKAEEDRPLEDVQAEAGNPQPSSEGVQAEAGNPRGGPNQPGQG
 .. *.* ***.* ***.* ***.* ***.* ***.* ***.* ***.*

pp21 1" MKSCQKMEGKPN---ESEPKEHEEPKPEEKPEEEKLEEEAKAKGTFRERLIQSLQE

HP10437 61' FKEDTPVRHLDP EEMIRGVDELERLREEIRRVNRKFMVMHWKQHSRSRYPVPCFRP
 ****.. ***.* **.*.****. *****.*.***. **

pp21 56" FKEDIHNRHLSNEDMFREVDEI---DEIRRVNRKLIVMRWKVNRRNHPYPYLM

HP10437 1' MQKSCEENEGKPNMPKAEEDRPLEDVPEAEGNPQPSSEGVSQEAEGNPRGGPNQPGQG

[illegible]

pp21 1" MKSCQKMEGKPN-----ESEPKEHEEPKPEEKPEEEKLEEEAKAKGTFRERLIQSLQE

HP10437 61' FKEDTPVRHLDPEEMIRGVDELERLREEIRRVNRKFMHMKQHSRSPYPVCFRP

[illegible]

pp21 56" FKEDIHRHLSNEDMFREVDEI ---DEIRRVNRKLIWRWKVNRNHPYPYLM

Fig. 13

HP10525 1' MELSAYLREKLQDLEAEHVEVEDTINRCSFRLVVSAKFEKPLLQHRHRLVNACL
 ... * * * * *
 SPAC8C9 1" MVNAQQLELLIQNTLEPTHEIQDM-SGGCGQNFVEIIVSPLFECKSTLARHRLVNHKL

 HP10525 61' AEELPHIHAFEQ-KTLTPDQWARERQK
 * *
 SPAC8C9 59" QEVIKDIHAFTQVRTLSFRHIR

Fig. 14

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HP10543 1' MAATEPILAAATGSPAAPPEKLEAGAGSSAPERNCVGSLLPEASPPAPEPSSPNAAVPEA
LEAP1 1" .. ** * * * *
        MAAPQPSQDPQSPAAPPEQEGAGDCA

HP10543 61' IPTPRAAASAALEPLGPAPVSVAPQAEAEARSTPGPAGSRLGPETFRQRFQFRYQDAA
LEAP1 28" * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
        APSPDSGSSPAPELPGAPAAINTAPYADAVLR---PGASRPGPETFRQRFQFRYQDAA

HP10543 121' GPREAFRQLRELSRQWLRPDIRTKEQIVEMLVQEQLLAILPEAAARRIRRRTDVIRITG
LEAP1 84" * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
        GPREAFRQLRELSRQWLRPDIRTKEQIVEMLVQEQLLAILPEAAARRIRRRADVIRITG

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Fig. 15

HP03090 1' MAARRALHFVFKVGNRFQTARFYRDVLGMKVLRRHEEFGCKAACNGPYDGKWSKTMVGF
 CEHYPO 1" MTARALHYVFKVANRAKTIDFFTNVLNMKVLRRHEEFGCEATCNGPYNGRWSKTMIGY
 HP03090 61' GPEDDHFVAELTYNYGVGDYKLGNDFMGITLASSQAVSNARKLEWPLTEVAEGVFETEAP
 CEHYPO 60" GSEDEHFVLEITYNYPIHKYELGNDYRAIVIDSDQLFEKVEKIN--HRKSGCGRLAVKDP
 HP03090 121' GGYKFYLNRSRSLPQSDPVLKVTLAVSDLQKSLNYWCNLLGMKIYEKDEEKQRALLGYADN
 CEHYPO 118" DGHEF--KIGKADQSPKVLRVQNVNVDLEKSKKYWNETLGMPIVEEKSSRIR--MSYGDG
 HP03090 181' QCKLELQGVKGGVDHAAAFGRIAFSCPQKELPDIEDLMKRENQKILTPLVSLDTPGKATV
 CEHYPO 174" QCELEIVKSQDKIDRKTGFGRIFAFSYPEDKLESLQDKIKSANGTIINELTLETPGKADV
 HP03090 241' QVVILADPDGHEICFVGDEAFRELSKMDPEGSKLLDDAMAADKSDWEFAKHNPCKASG
 CEHYPO 234" QVVILADPDGHEICFVGDEGFRALSKIDDKAESSELKEQIKKDDSEKWI

Fig. 16

HP03145 1' MLGSRAAGFARGLRALALAWLPWGRGRSFALARAAAGPHGGDLQPPACPEPRGRQLSLSA
 SCCOQ2 1" MIIKPIASPARYFLRTPSWSAVAIFQAVKIKPLQLRTNSSNSVTPNLIIPSK
 HP03145 61' AAVVDSAPRPLQPYLRIMRLDKPIGTWLLYLPCTWSIGLAA---EPGCFPDWYMLSLFGT
 SCCOQ2 53" KSWKDLFSKRWQYYAEISRAGSPTGTYYLLYSPCTWSILMAAYAYDSSLVNVTKMLALFGV
 HP03145 118' GAILMRGAGCTINDMWDQDYDKKVTRTANRPIAAGDISTFQSFVFLGGQLTALGVLLCL
 SCCOQ2 113" GSFLMRGAGCVINDLWDRELDKAKVERSKSRPLASGKLSVRQAISSLVQLTASLGILLQL
 HP03145 178' NYYSIALGAGSLLLVITYPLMKRISYWPQLALGLTFNWGALLGWSAIGK-SC-DPSVCLP
 SCCOQ2 173" NPYTIKLGVASLVPVCIYPAMKRITYYPQVVVLGLTFGYGAVMGWPALLAGEACMNWSVVAP
 HP03145 236' LYFSGVMWTLIYDTIYAHQDKRDDVLIGLKS TALRFGENTKFWLSGFSVAMLGALSLVG
 SCCOQ2 233" LYLSTISWIVLYDTIYAHQDKRDDVKANIYSTALRFGDNTKPVLCGLAALQIATLATAGI
 HP03145 296' NSGQTAPYYA-ALGAVGAHLTHQIYTLDIHRPEDCWNKFISNRTLGLIVFLGIVLGNLWK
 SCCOQ2 293" MNGQGPVFFYTLGVAGAAYRLSSMIYKVDLDDPKDCFRWFKRNSNTGYLVAAAIALDWLAK
 HP03145 355' EKKTDKTKKGIENKIEN
 SCCOQ2 353" SFIYDS

Fig. 17

HP03185 361' IYQEMAKLDAK
*****.
MH2A1.2 361" IYQEMAKLDAN

Fig. 18

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HP03324	1'	MALCALTRALRSNLAPPTVAAPAPSLFPAAQMMNGLLQQPSALMLLPCRPVLTVALN
BRPL2	1"	MGLKRFPVTPGRRFMVI
HP03324	61'	ANFVSWKSRTKYTITPVKMRKSGGRDHTGRIRVHGIGGGHKQRYRMIDFLRFRPEETKSG ..***.* **.* **.* **.* **.* **.* **.* **.*
BRPL2	19"	SDFS DITKTEPEKSL L APLKKTGGRNHHGRVTVRHRGGGHHKRRYRIIDFKRY----DKAG
HP03324	121'	PFEKVIQVRYDPCRSADIALVA-GGSRKRWIIATENMQAGDTILNSNHIGRMAVAAREG .***... *** *** ***. ... **.* **.* **.* **.* **.* **.*
BRPL2	75"	-IPAKVLAIEYDPNRSARIALLLLYADGEKRYIILAPKGVNVGDTLMSGPD---AEIRP--G
HP03324	180'	DAHPLGALPVGTLINNVESEPGRGAQYIRAAGAGNVRNSRPSIQR .* **.* **.* **.* **.* **.* **.* **.*
BRPL2	129"	NALPLEKIPVGTLVHNVEFTPGKGGQIARAAGTYCQIMAKEGNVALLRMPSPGELRKVHIK

Fig. 19

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HP10648 181' LTPRPGSPRGQHEPSKPPPAGEVTGTGGFAGAKKRGSSSQAPASKKLNKEELPVIKGP

CEY40B1B 1" MSTGANLLVMNDTC

HP10648 241' KSGRVWKDRSKKRFSQMLQDKPLRTSWQRKMKERQERKLAKDFARHLEEEKERRRQEKQ

CEY40B1B 15" KSNRWKTKQEKKHSEIKKVKTLKSTWDKMKELKAKDMVKRVQDNIREKQVQERQEKKE

HP10648 301' RRAENLKRRLENERKAEVVQVIRNPAKLKRAKKQLRSIEKRDTLALLQKQPPQPAKI

CEY40B1B 75" RKVEQEKRRLENERKAEIVQKITKIHKLKKTKKRQLRSIQMRDTTQVTK

Fig. 20

HP10162	1'	MEPQERETQVAAWLKKIFGDHP	IPQYEVNPRTEILHLSERNVRDRDVYLVI	EDLKKQ
RNUNK	1"	MAALEEKASQVAEWLKKIFGDHP	IPQYEMNARTTEILYHLSERNVRDRDVNLVIE	DLRPP
HP10162	61'	KASEYSEAKYLQDLIMESVNFSPANL	SSTGSRYNALVDSVALETKDTSLASF	IPAVN
RNUNK	61"	KASEYSEAKRLEDFLIMESVNFSPANL	SNTGSRFLNALVDSIALEIKDTSLASF	IPAVN
HP10162	121'	DLTSDLFRTKSKSEEIKIELEKLEKNLTATLVLEKCLQEDVKKAEHLHLSERAKVDNRRRQ		
RNUNK	121"	DLTSDLFRTKSKSEEIKLELGKLEKNLTATLVLEKCLREDLKKADVHLSAERAKAEGRLQ		
HP10162	181'	NMDFLKAKESEFRFGIKAAEEQLSARGMDASLSHQSLVALSEKLARLKQQTPLKKKLES		
RNUNK	181"	NMDFLKAKEAFRFGIRAAEEQLSRGMDASLSHRSLVALSDKLSELKQQTPLKKKLES		
HP10162	241'	YLDLMPNPSLAQVKIEAKRELD	SIEAELTRRRVDM	MEL
RNUNK	241"	YLDLMPNPSLAQVKIEAKRELD	IAEALTKKVD	MEL

Fig. 21

HP10334 1' MSGLRVYSTSVTGSREIKSQSQSEVTRILDGKRIRQYQLVDISQDNALRDEM---ALAGNP
HSSH3 .*** .*.*** .*** .*.*** .*.*** .*.*** .*.*** .*.*** .*.***
1" MVIRVYIASSSGSTAIAKKKQDVLGFLFLEANKIGFEEKDIAANEENRKMRENVPENSRP
HP10334 58' KAT---PPQIVNGDQYCGDYELFVEAVEQNTLQEFLLKLA
HSSH3 .. **** *...*** .*** .*** .*** .*** .*** .*** .***
60" ATGYPLPPQIFNESQYRGDYDAFFEAARENNAVYAFGLTAPPGSKEAEVQAKQQA

Fig. 22

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HP10532 1' MAGSEELGLREDTLRVLAFLRRGEAAGSPVTPPRSPAQEEPTDFLSRLRRCCLPCSLGR
HSBBK *****
1" MAGSEELGLREDTLRVLAFLRRGEAAGSPVTPP-SPAQEEPTDFLSRLRRCCLPCSLGR

HP10532 61' GAAPSESPRCSLPIRPCYGLEPGPATPDFYALVAQRLEQLVQEQLKSPSPPELQGGPPST
HSBBK *****
60" GAAPSESPRCSLPIRPCYGLEPGPATPDFYALVAQRLEQLVQEQLKSPSPPELQGGPPST

HP10532 121' EKEAILRRLVALLLEEEAEVINQK-----
HSBBK *****

120" EKEAILRRLVALLLEEEAEVINQKASDPALRSKLVRLSSDSFARLVELFCSRDDSSRPSR

HP10532 181' -----EGILAV
HSBBK *****

180" ACPGPPPPSPEPLARLALAMELSRRVAGLGGTLAGLSVEHVHSFTPWIAHGGWEGILAV

HP10532 241' SPVDLNLPLD
HSBBK *****
240" SPVDLNLPLD

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Fig. 23

HP10559 1' MPVKKRKSPGVAAVAEDGGLKKCKISSYCRSQPPARLISGE
 KIAA 61" QTGSLRSCSSDCFNKVMPPRRKRR-----PASGDDLSAKKSRHDSMYRKYDSTRIKTEE
 HP10559 44' EHFSSKKCLAWFYEYAGPDEVVGPEGMEKFCEDIGVEPENIIMLVLAWKLEAESMGFFTK
 KIAA 116" EAFSSKRCLEWIFYEYAGTDDVVGPEGMEKFCEDIGVEPENVMVLVLAWKLDAQNMGYFTL
 HP10559 104' EEWLKGMTISLQCDCTEKLQNKDFELRSQNDISSFKNIYRYAFDFARDKDQORSLDIDTAK
 KIAA 176" QEWLKGMTISLQCDTTEKLRLNTLDYLRSLNDSTNFKLLIYRYAFDFAREKDQORSLDINTAK
 HP10559 164' SMLALLIGRTWPLFSVFFYQYLEQSKYRVMNKDQWYNVLEFSRTVHADLSNYDEDEDGAWPVL
 KIAA 236" CMLGLLLGKIWPLFPVFHQFLEQSKYKVINCKDQWCNVLEFSRTINLDSNYDEDEDGAWPVL
 HP10559 224' LDEFVEWQKVRQTS
 KIAA 296" LDEFVEWYKDKQMS


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HP10562 61' QESEPEDFLKLFIDPNEVYCSEASPGSDSGISEDPCHPDPPAPRATSSPMLYEVVYEAG
LZIP 1" MELELDAGDQDLLAFLLEESGDLGTAPDEAVRAPLDWALPLSEVPDWEVDDLL
HP10562 121' ALERMQGETGPNVGLISIQLDQWSPAFMVPDSCMVSELPFDAHAHILPRAGTVAPVPCTT
LZIP 54" LCSLLSPPASLNILSSSNPCLVHHHTYSLPRETVSMDLESESCRKEGTQMT PQHMEELA
HP10562 181' LLPCQTLFTDEEKRLLGQEGVSLPSHLPLTKAERVVKVRRKIRNKQSAQDSRRRRKKE
* *****.***.***.***.*****.***.*****.***.***.***
LZIP 114" EQEIALVLTDEEKSLLKEGLILPETPLTKTTEEQILKRVRRKIRNKRSAQESRRKKKV
HP10562 241' YIDGLES RVAACSAQNQELQKKVQELERHNISLVAQLRQLTLIAQTSNKAQSTC VLI
*..***** ..***.***.***.***.***.***.***.***.***.***.***.***
LZIP 174" YVGGLES RVLK YTAQNME LQNKVQLLEE QNL SLLDQLRK LQAMVIEISNKTSSSSTC ILV
HP10562 301' LLFSLAL IILPSFPQSR---PEAGSE DYQPHGVT SRN--ILTHKDV TENLETQV VES
**.*...*.***.***.***.***.***.***.***.***.***.***.***
LZIP 234" LLVSFCLLLVPAMYSSDTRGSLPAEHGVL SRQLRALPS EDPYQLEL PALQSEVPKDS THQ
HP10562 355' RLREPPGAKDANGSTR T LLEKMGKPRPSGRIRSVLHAD EM
.*...*.***.***.***.***.***.***.***.***.***.***.***
LZIP 294" WLDGSDCVLQAPGNTSCLLHYMPQAPSAEPPL EWFPFDL FSEPLCRGPILPLQANLTRKG

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Fig. 26

HP10498 1' MATPSLRGRLARFGNRPKPVLPKNKPLILANRV-GERRREKGEATCITEMSVVMA
 CEC24 1" MMFSSPLLKEKALARGKSIYPKVAVFSEILPLASKNRVQAGQKPRAASSCTQELQALFG
 * * * * * *
 HP10498 55' CWKQNEFRDDACRKEIQGFLDCAAR-AQEARKMR--SIQETLGESGSLLPNKNLKLQRF
 * * . * * * . * . . . * * * *
 CEC24 61" CLKKWEFDDVPCSKQHTLYMDCVHKGAEEAAAYRDATRKGTLGESGAGGKQSMTSAQFNK
 HP10498 112' PNKPYL
 CEC24 121" IQKLFPQPDLGKQPYRQMKRLPTQDYADDTFHRKHWSGKRS

Fig. 27

HP10505	1'	MAKHLKFIARTVMVQEGNVESAYRTLNRILTMDGLIEDIKHRRYYEKPCCRRRQRESYERC
CEF29	1"	<div style="display: flex; justify-content: space-between;"> <div>***...*. * .</div> <div>***...*. * .</div> </div>
HP10505	61'	<div style="display: flex; justify-content: space-between;"> <div>***...*. * .</div> <div>MVQNNDVDGAFGLNRLMDSEGMLKIIRRTQFYQKPYMQRKTLSEAS</div> </div>
CEF29	49"	<div style="display: flex; justify-content: space-between;"> <div>RIYNMEMARKINFLMRKNRADPWQGC</div> <div>TAIFNEDMNRKKFLVRKNRPDKHPGQVTS</div> </div>

Fig. 28

HP10515 1' MFLTAL-LWRGRIPGROWIGKRRRPRFVSLRAKQNMIRRLIEIAENHYWLSMPYMTREQE
* * * . * . . * * . * * . *

DM63B 1" MHILTINLFKKTVPGHIFRGKRRLVKPVSQRAMDTLTREYERQEQVMLLLRHPYLTMEQS

HP10515 60' RGHA-AVRREAFEA--IKAAATSKFPHRFIADQLDHLNVTKKWS
*** * * *

DM63B 61" FGHAKELQKREKLVARWTDEOTLRKMKPHTTIEERLNQLKIKEAWD

Fig. 29

HP01124	1'	MGTEKESPEPDCQKQFQAASVQNLPKNGSYRPSYEMLRFYSYKQATMGPCLVPRPG
HSACBP	1'	MSQAEFEKAAEEVRHL----KTKPSDEMLFIYGHYKQATVGDINTERPG
HP01124	60'	FWDPIGRYKWDANSLGKMSREEAMSAYITEMKLVAQKVIDTVPLGEVAEDMFGYFEPLY
HSACBP	47"	MLDFTGKAKWDANWELKGTSKEDAMKAYINKVEELKKKYGI

[illegible]

Fig. 31

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HP10101 1' MKA VKSERERGSRRRRHRDGDWVLPAGVVVKQERLSPEVAPPAHRRPDPHSGSPSPPTSEEP
HP10101 60' ARSGHRGNRARGVSRPSPKKKNKASGRRSKSPRSKHNRSPPHSHSTVKVKQEREDHPRRGRE
CEC32E8 1' MGRDSPDRRRHRDRSPERRRRSRSRDRQTRRD-T
HP10101 121' DRQHREPSEQEHRRA RNSDRDRHRGHSQRRTSNRPGSGQGQGRDRDTQNLQAQEEERE
CEC32E8 36" RRDDSPKIKREVKEEQFSDNDSPPRRRRDRGRRDRDRDRNRDRD-RDHRDDRGDRDRDR
HP10101 181' FYNARRREHRQRNDVGGGSESQELVPRPGNNKEKEVPAKEKPSFELSGALLEDTNTR
CEC32E8 95" NF--RRPDPVREDGKQYGLEKKEENWGKPEEPAKEK-----EKVNLGTSGALTEDTNTFR
HP10101 241' GVVIKYSEPPEARIPKKRWRLYPFKNDEVLPVMIYHRQSAVLLGRHRRRIADIPIDHPSCS
CEC32E8 148" GVVIKYNEPPEAKPNARWRLYPFKGEESLQVLYIHRQSAVLLIGRDHKIADIPVDHPSCS
HP10101 301' KQHAVFQYRLVEYTRADGTVGRRVKPYIIDLGSGNGTFLNNKRIEQRYYELKEKDLKF
CEC32E8 208" KQHAVLQFRSMFPTRDDGTKARRIMPYIIDLGSGNGTFLNEKKIEPQRYIELQEKDMLKF
HP10101 361' GFSSREYVLLHESSTSEIDRKODEDEEEEEEVS
CEC32E8 268" GFSTREYVVMKEREITEEELAEGEDVVKKEES

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HP10370	1"	MEYDEKLARFRQAHNLNPNKQSGRQHEQGPGEEVDPDVTPEALPELPPGPEPE
DMCG115	1"	MSSWKDSLTSIPGTVAQLINESASNLLHASSTLGSITVGLGGSGTSGSGSEAGGSESGPQ
HP10370	55'	RCPERVMDLGLSEDHFSRPVGLFLASDVQQLRQAIIECKQVILELPEQSEKQKDAVVRLI
DMCG115	61"	GAEYRALPIPASLVREQWRLIFTSANIQLQAAIAHCRDLVLLSEELSEERRWLVRHLV
HP10370	115'	HLRLKLQELKDPNE-----DEPNIRVLEHRF-----YKEKSKSVKQTCDK
DMCG115	121"	DLRYSLQELEEAQEQHSLSSDMVVMNAIRAVVGHFVPHPHGKRNRLQAAAKRNYCDH
HP10370	156'	CNTIYGLIQTWYCTGCTGYRCHSKCLNLISKPCVSSKVSHQAEYELNICPETGLDSQDY
DMCG115	181"	CTTIWSVVQNSYVCSDCGFLVHQKIDGVKRVCAHVLVSRQHPISEICPEIGLASQGY
HP10370	216'	RCAECRAPISLRGVPSPEARQCDYTGQYYCSCHWNDLAVIPARVVHWNDFEPRKVSRCSM
DMCG115	241"	KCAECQTMNLKNTWIEPRLCDYGLYPCRCWNDSNFIPARIHWNDFSRRVSR TAL
HP10370	276'	RYALMVRPVLRLREINPLFSYVEELVEIRKLQDILLMKPYFTCREAMEARLL-LQ
DMCG115	301"	QEIRLFNLKPLIRLEEDNPKLFVFEKLCVKKLRQLVHMRHYLAACKIASLKLVDQO
HP10370	335'	LQDRQHFEVNDEMYSVQDLLDVHAGRLGCSLTEIHTLFAKHIKLDCERCQAKGFVCELCR
DMCG115	361"	LGVRRHLAQNEFYLSLSDLSQVESGALSEFLQGVFKAFNDHIR-SCPMCLAQAYICEIC
HP10370	395'	EGDVLPFFDSHTSVCADCSAVFHRDCYVDNSTTCPKCARLLSLRKQSLFQEPGPDVEA
DMCG115	420"	NNEVTFPFFDDGCIKCDQCNISIFHRVCLTRKNMICPKCIRIQERRQLDMMKSTEDDDDD

Fig. 33

HP10427 1' MAGPAAAFRRRLGALSGAAALGFASYGAH--GAQFPDAYGKELFDKANKHHFLHSLALIG
 ... ***** * .. ** *****.
 CEY106G 1" MSPIIRLAGLSGAVAISLGAYGSHVLRDNPISIDERRRTAFDTASRYHLIHSIALLA

 HP10427 58' VPHCRKPLWAGLLLIASGTTLFCFTSFYYQALSGDPSIQTLAPAGGTLTLLGLWLALAL
 * * ** * .. ** * * * *
 CEY106G 57" SPAARFPLVTAGLFTAGITLFCGPCYHYSISGVETTRKYTPIGGVTLIIAWLSFIL


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HP10516 1' MAGTGLLALRTLPGPSWVRGSGPSVLSRLQDAAVVRPGFLSTAEETLSRELEPELRRRR
      . . . . . * * * * * * * * * * * *
DMCG141 1" MRIITDFISEPEEQQLHEEIEPYMSRLR

HP10516 61' YEYDHWDAAIHGFRETEKSRWSEASRAILQRVQAAFGPGQTLLSSVHVLDLEARGYIKP
      * * * * * . . . . . * * * * * * * * * * *
DMCG141 29" YEFDHWDDAIHGFRETERKKWFKNREILERVQVAF--DGAVMPYVHILDLPDGVIKP

HP10516 121' HVDSIKFCGATIAGLSLSPVMRLVHT-----QEPG
      * * * * * . . . . . * * * * * *
DMCG141 87" HVDS TRYCGNTISGISLSDSVMLVRTDEQRYQQSSGTATDPNSQSEPDAAVYRHQPE
      * * * * *

HP10516 153' EWL-----ELLEPGSLYILRGSAFYDFSHEILRDEESFFGERRIPRGRRIISVICRSLP
      * . . . . * * * * * . . . . * * * * * *
DMCG141 147" ASLKNFYADILLPRRSLYIMSHYARVFTHEILAKEHSQFQALVPRTRRIISII CRNEP

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Fig. 35

HP10580	1'		MKKFFQEFKADIKFK
DMCG546	61"	TLKVLIVLLGTCVLGYSWSIYGKVI	TEKFFVRPSTLKEIEELKLSKAAAFKLNLTGS
HP10580	16'	SAGPGQKLKESVGEKAHKEKPNQ--	PAPRPPRQGP
DMCG546	121"	GMGTGHLN	SPKQETPSSSRQKYEA
HP10580	74'	TSQDTIRNQVRKELQAEATVSGSP-	EAPGTNVVSEPREGSA-HLAVPGVYFTCPL-TGA
DMCG546	180"	TSLSAVKAQA	KRELEAEERRQREEAMGTPSTSTSTASGGDTRNLACEGVFFRCPLISEE
HP10580	131'	TLRKQORDACIKEA	ILLHFSTDPVAASIMKIYTFNKDQDRVKLGVDTLAKYLDNIHLHPE
DMCG546	240"	ILPKSVWKVRIKEFLYQQLEAD	RGLTACLIHNCN-VKEKADECIATLIRYLENLIKNPE
HP10580	191'	EEKYRKIKLQNKVFQERINCL	EGTHEFFEAIGFQKVLPAQDQEDPEEFYVLSETTLAQP
DMCG546	299"	EEKFC	KIRMSNKFSEKVRVVEGALDVLQAAGFNEV-----QIDGEPFLLTWKEQTEKD

Fig. 35-1

35/1/35

HP10580 251' QSLERHKEQLLAEPVRAKLDQRQRRVFQPSPLASQFELPGDFFNLTAEEIKREQRLRSEA
* * * * *
DMCG546 353" LDLPTLVEALKSSEIIPLELDNRNIKVLLPSQ-ACRVALPDEFYRLSPEEIKKEQQQLRSEA
* * * * *

HP10580 311' VERLSVLR TKAMREKEEQ RGLRKYN YTL LRVRLPDGCLLQGT FYARERLGAVYGFVREAL
... * * * * *
DMCG546 412" IAQSQMLR TKAMREKEEQ RNLRMRYALVRVKFPNGLFIQGT FNVYEKISDVFEFVQSCL
* * * * *

HP10580 371' QSDWLPFELLASGGQKLSEDE-NLALNECGLVPSALLTFSSWDMAVLEDIKAAGAEPSIL
... * * * * *
DMCG546 472" ADESLDFSLVSNSDGKLGDEDELEKTL YDCKLI PNTLLLF SANDTPAPLQTDINYLKEDLL
* * * * *

HP10580 430' KPELLSAIEKLL

DMCG546 532" MLVQAM